

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rag.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:13:52 ; Search time 105.264 Seconds
(without alignments)
196.180 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.....KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	255	100.0	47	3 AAY77405	Aay77405 Rainbow t
2	255	100.0	47	7 ADF56463	Adf56463 Rainbow t
3	244	95.7	47	7 ADD67520	Add67520 Rainbow t
4	244	95.7	47	8 ADP82542	Adp82542 Rainbow t
5	231.5	90.8	74	3 AAY77407	Aay77407 Rainbow t
6	231.5	90.8	74	7 ADF56465	Adf56465 Rainbow t
7	220.5	86.5	74	7 ADD67518	Add67518 Rainbow t

8	220.5	86.5	74	8	ADP82540	Adp82540	Rainbow t
9	198.5	77.8	186	2	AAR72472	Aar72472	Flatfish
10	198.5	77.8	186	8	ADV95289	Adv95289	Rockfish
11	172	67.5	35	3	AAV77404	Aay77404	Rainbow t
12	172	67.5	35	7	ADD67521	Add67521	Rainbow t
13	172	67.5	35	7	ADF56462	Adf56462	Rainbow t
14	172	67.5	35	8	ADP82543	Adp82543	Rainbow t
15	168.5	66.1	62	3	AAV77406	Aay77406	Rainbow t
16	168.5	66.1	62	7	ADD67519	Add67519	Rainbow t
17	168.5	66.1	62	7	ADF56464	Adf56464	Rainbow t
18	168.5	66.1	62	8	ADP82541	Adp82541	Rainbow t
19	168.5	66.1	176	2	AAR88089	Aar88089	Rainbow t
20	132	51.8	105	4	AAE02452	Aae02452	Rabbit li
21	132	51.8	105	4	AAE02450	Aae02450	Human liv
22	132	51.8	105	4	AAE02456	Aae02456	Rabbit li
23	132	51.8	105	5	AAU10562	Aau10562	Human ins
24	132	51.8	105	5	AAU10564	Aau10564	Rabbit in
25	132	51.8	105	7	ABR63172	Abr63172	Rabbit li
26	132	51.8	105	7	ABR63170	Abr63170	Human liv
27	132	51.8	105	9	ADZ58808	Adz58808	Human mat
28	132	51.8	119	1	AAP60578	Aap60578	Human pre
29	132	51.8	130	9	AEB70451	Aeb70451	Insulin-l
30	132	51.8	137	4	AAU09067	Aau09067	Human ins
31	132	51.8	137	8	ADU46866	Adu46866	Insulin-l
32	132	51.8	137	9	AEB70455	Aeb70455	Insulin-l
33	132	51.8	137	9	AEB70450	Aeb70450	Insulin-l
34	132	51.8	153	2	AAR83803	Aar83803	Insulin-l
35	132	51.8	153	2	AAW69733	Aaw69733	Human IGF
36	132	51.8	153	2	AAW57882	Aaw57882	Human IGF
37	132	51.8	153	5	AAU84284	Aau84284	Human end
38	132	51.8	153	5	AAU84341	Aau84341	Protein I
39	132	51.8	153	6	ADA26451	Ada26451	Human ins
40	132	51.8	153	7	ADC59343	Adc59343	Human ins
41	132	51.8	153	7	ADD25494	Add25494	Binding d
42	132	51.8	153	7	ADP65213	Adp65213	Human ins
43	132	51.8	153	8	ADH10374	Adh10374	Human ins
44	132	51.8	153	8	ABO84602	Abo84602	Human can
45	132	51.8	153	8	ADS73976	Ads73976	Insulin-l

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:23:52 ; Search time 26.0248 Seconds
(without alignments)
149.310 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.....KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	255	100.0	47	2	US-09-120-818-2
2	255	100.0	47	2	US-09-609-642-2
3	255	100.0	47	2	US-09-669-642-2
4	231.5	90.8	74	2	US-09-120-818-4
5	231.5	90.8	74	2	US-09-609-642-4
6	231.5	90.8	74	2	US-09-669-642-4
7	172	67.5	35	2	US-09-120-818-1
8	172	67.5	35	2	US-09-609-642-1
9	172	67.5	35	2	US-09-669-642-1
10	168.5	66.1	62	2	US-09-120-818-3

11	168.5	66.1	62	2	US-09-609-642-3	Sequence 3, Appli
12	168.5	66.1	62	2	US-09-669-642-3	Sequence 3, Appli
13	168.5	66.1	176	1	US-07-953-230A-9	Sequence 9, Appli
14	132	51.8	105	2	US-09-852-261-10	Sequence 10, Appl
15	132	51.8	105	2	US-09-852-261-14	Sequence 14, Appl
16	132	51.8	119	6	5405942-1	Patent No. 5405942
17	132	51.8	127	2	US-09-617-389B-18	Sequence 18, Appl
18	132	51.8	137	1	US-07-953-230A-10	Sequence 10, Appl
19	132	51.8	152	2	US-08-950-720A-9	Sequence 9, Appli
20	132	51.8	153	1	US-08-219-878A-1	Sequence 1, Appli
21	132	51.8	153	2	US-09-917-254-82	Sequence 82, Appl
22	132	51.8	153	2	US-09-919-497-74	Sequence 74, Appl
23	132	51.8	153	4	PCT-US93-04329-1	Sequence 1, Appli
24	132	51.8	156	2	US-09-142-583A-11	Sequence 11, Appl
25	132	51.8	184	2	US-09-949-016-7523	Sequence 7523, Ap
26	132	51.8	191	2	US-08-989-251-41	Sequence 41, Appl
27	132	51.8	191	2	US-09-340-250-41	Sequence 41, Appl
28	132	51.8	191	2	US-09-528-108-41	Sequence 41, Appl
29	132	51.8	191	2	US-09-921-398-41	Sequence 41, Appl
30	132	51.8	191	2	US-10-280-826-41	Sequence 41, Appl
31	125	49.0	105	2	US-09-852-261-12	Sequence 12, Appl
32	85.5	33.5	110	2	US-09-852-261-2	Sequence 2, Appli
33	83	32.5	111	2	US-09-852-261-6	Sequence 6, Appli
34	83	32.5	121	2	US-09-142-583A-4	Sequence 4, Appli
35	79.5	31.2	111	2	US-09-852-261-4	Sequence 4, Appli
36	74	29.0	19	2	US-09-142-583A-6	Sequence 6, Appli
37	61.5	24.1	204	2	US-09-134-001C-4814	Sequence 4814, Ap
38	59	23.1	508	1	US-08-818-024-3	Sequence 3, Appli
39	59	23.1	508	2	US-09-334-775A-3	Sequence 3, Appli
40	58.5	22.9	388	2	US-09-270-767-58024	Sequence 58024, A
41	58.5	22.9	1113	2	US-09-270-767-42704	Sequence 42704, A
42	57.5	22.5	407	2	US-09-538-092-656	Sequence 656, App
43	57	22.4	588	1	US-08-391-615-5	Sequence 5, Appli
44	56.5	22.2	191	2	US-09-489-039A-13754	Sequence 13754, A
45	56.5	22.2	1064	2	US-09-926-820-1	Sequence 1, Appli

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:24:43 ; Search time 92.4463 Seconds
(without alignments)
212.426 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.....KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	244	95.7	47	4	US-10-100-492-4	Sequence 4, Appli
2	220.5	86.5	74	4	US-10-100-492-2	Sequence 2, Appli
3	198.5	77.8	186	6	US-11-049-518-27	Sequence 27, Appl
4	172	67.5	35	4	US-10-100-492-5	Sequence 5, Appli
5	168.5	66.1	62	4	US-10-100-492-3	Sequence 3, Appli
6	132	51.8	105	3	US-09-852-261-10	Sequence 10, Appl
7	132	51.8	105	3	US-09-852-261-14	Sequence 14, Appl
8	132	51.8	105	5	US-10-504-078-10	Sequence 10, Appl
9	132	51.8	105	5	US-10-504-078-14	Sequence 14, Appl
10	132	51.8	105	5	US-10-688-821-53	Sequence 53, Appl

11	132	51.8	127	4	US-10-700-725-18	Sequence 18, Appl
12	132	51.8	130	6	US-11-049-518-25	Sequence 25, Appl
13	132	51.8	137	4	US-10-251-661-8	Sequence 8, Appli
14	132	51.8	153	3	US-09-919-497-74	Sequence 74, Appl
15	132	51.8	153	3	US-09-861-101-5	Sequence 5, Appli
16	132	51.8	153	4	US-10-136-639-3	Sequence 3, Appli
17	132	51.8	153	4	US-10-207-655-55	Sequence 55, Appl
18	132	51.8	153	4	US-10-460-550-5	Sequence 5, Appli
19	132	51.8	153	4	US-10-706-791-2	Sequence 2, Appli
20	132	51.8	153	5	US-10-851-921-2	Sequence 2, Appli
21	132	51.8	153	5	US-10-461-862-68	Sequence 68, Appl
22	132	51.8	153	5	US-10-460-550-5	Sequence 5, Appli
23	132	51.8	153	5	US-10-287-436A-455	Sequence 455, App
24	132	51.8	153	5	US-10-287-436A-1154	Sequence 1154, Ap
25	132	51.8	153	5	US-10-798-896-4	Sequence 4, Appli
26	132	51.8	191	3	US-09-921-398-41	Sequence 41, Appl
27	132	51.8	191	3	US-09-967-768-41	Sequence 41, Appl
28	132	51.8	191	4	US-10-280-826-41	Sequence 41, Appl
29	132	51.8	191	6	US-11-046-099-41	Sequence 41, Appl
30	127	49.8	105	4	US-10-238-114-3	Sequence 3, Appli
31	127	49.8	153	4	US-10-238-114-2	Sequence 2, Appli
32	125	49.0	105	3	US-09-852-261-12	Sequence 12, Appl
33	125	49.0	105	5	US-10-504-078-12	Sequence 12, Appl
34	88.5	34.7	77	4	US-10-100-492-1	Sequence 1, Appli
35	88.5	34.7	195	4	US-10-443-466A-20	Sequence 20, Appl
36	88.5	34.7	195	4	US-10-706-791-3	Sequence 3, Appli
37	88.5	34.7	195	5	US-10-461-862-66	Sequence 66, Appl
38	86	33.7	133	4	US-10-161-088-2	Sequence 2, Appli
39	86	33.7	133	5	US-10-461-862-63	Sequence 63, Appl
40	85.5	33.5	110	3	US-09-852-261-2	Sequence 2, Appli
41	85.5	33.5	110	5	US-10-504-078-2	Sequence 2, Appli
42	83	32.5	111	3	US-09-852-261-6	Sequence 6, Appli
43	83	32.5	111	5	US-10-504-078-6	Sequence 6, Appli
44	80	31.4	104	6	US-11-049-518-17	Sequence 17, Appl
45	79.5	31.2	111	3	US-09-852-261-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:25:58 ; Search time 13.2066 Seconds
(without alignments)
156.599 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.....KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

- 1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	255	100.0	47	6	US-10-647-732A-2	Sequence 2, Appli
2	231.5	90.8	74	6	US-10-647-732A-4	Sequence 4, Appli
3	172	67.5	35	6	US-10-647-732A-1	Sequence 1, Appli
4	168.5	66.1	62	6	US-10-647-732A-3	Sequence 3, Appli
5	132	51.8	105	7	US-11-228-458-10	Sequence 10, Appl
6	132	51.8	105	7	US-11-228-458-14	Sequence 14, Appl
7	132	51.8	130	7	US-11-043-788-222	Sequence 222, App
8	132	51.8	137	7	US-11-043-788-221	Sequence 221, App

9	132	51.8	137	7	US-11-043-788-226	Sequence 226, App
10	132	51.8	153	7	US-11-043-788-223	Sequence 223, App
11	132	51.8	153	7	US-11-043-788-228	Sequence 228, App
12	132	51.8	153	7	US-11-244-925-4	Sequence 4, Appli
13	132	51.8	567	6	US-10-954-468-8	Sequence 8, Appli
14	132	51.8	574	6	US-10-954-468-4	Sequence 4, Appli
15	132	51.8	580	6	US-10-954-468-6	Sequence 6, Appli
16	132	51.8	587	6	US-10-954-468-2	Sequence 2, Appli
17	132	51.8	615	6	US-10-954-468-7	Sequence 7, Appli
18	132	51.8	622	6	US-10-954-468-3	Sequence 3, Appli
19	132	51.8	628	6	US-10-954-468-5	Sequence 5, Appli
20	132	51.8	633	6	US-10-954-468-1	Sequence 1, Appli
21	125	49.0	105	7	US-11-228-458-12	Sequence 12, Appl
22	88.5	34.7	195	7	US-11-043-788-220	Sequence 220, App
23	88.5	34.7	195	7	US-11-043-788-227	Sequence 227, App
24	85.5	33.5	110	7	US-11-228-458-2	Sequence 2, Appli
25	85.5	33.5	139	7	US-11-043-788-224	Sequence 224, App
26	85.5	33.5	142	7	US-11-043-788-225	Sequence 225, App
27	83	32.5	111	7	US-11-228-458-6	Sequence 6, Appli
28	79.5	31.2	111	7	US-11-228-458-4	Sequence 4, Appli
29	74	29.0	19	7	US-11-043-788-487	Sequence 487, App
30	55.5	21.8	121	6	US-10-678-790-63	Sequence 63, Appl
31	55.5	21.8	238	7	US-11-194-890-12	Sequence 12, Appl
32	55.5	21.8	267	7	US-11-194-890-11	Sequence 11, Appl
33	54	21.2	948	6	US-10-523-477-14	Sequence 14, Appl
34	54	21.2	964	7	US-11-024-959-477	Sequence 477, App
35	53	20.8	643	7	US-11-137-465-54	Sequence 54, Appl
36	53	20.8	653	7	US-11-137-465-55	Sequence 55, Appl
37	52.5	20.6	373	7	US-11-188-298-370	Sequence 370, App
38	52.5	20.6	1112	7	US-11-188-298-16876	Sequence 16876, A
39	52	20.4	438	7	US-11-024-959-342	Sequence 342, App
40	52	20.4	663	7	US-11-087-099-7915	Sequence 7915, Ap
41	52	20.4	723	7	US-11-072-512-2246	Sequence 2246, Ap
42	52	20.4	2444	7	US-11-188-298-17072	Sequence 17072, A
43	51.5	20.2	107	6	US-10-678-790-61	Sequence 61, Appl
44	51.5	20.2	122	6	US-10-678-790-60	Sequence 60, Appl
45	51.5	20.2	507	6	US-10-330-773-187	Sequence 187, App

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rpr.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:19:02 ; Search time 19.0331 Seconds
(without alignments)
237.596 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.....KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	255	100.0	161	2	C54270	insulin-like growt
2	231.5	90.8	188	2	A54270	insulin-like growt
3	231.5	90.8	188	2	B54270	insulin-like growt
4	191.5	75.1	155	2	C44012	insulin-like growt
5	172	67.5	149	2	D54270	insulin-like growt
6	168.5	66.1	176	2	A41396	insulin-like growt
7	168.5	66.1	176	2	A46244	insulin-like growt
8	140	54.9	153	2	A41399	insulin-like growt
9	132	51.8	137	1	IGGP1	insulin-like growt
10	132	51.8	137	2	A36552	insulin-like growt
11	132	51.8	153	1	IGHU1	insulin-like growt
12	131	51.4	153	2	A36079	insulin-like growt

13	128	50.2	153	2	S12825	insulin-like growt
14	127	49.8	138	2	S22878	insulin-like growt
15	127	49.8	153	1	IGBO1	insulin-like growt
16	127	49.8	154	2	JC2483	insulin-like growt
17	127	49.8	154	2	A33390	insulin-like growt
18	125	49.0	127	2	B40912	insulin-like growt
19	125	49.0	127	2	A25540	insulin-like growt
20	125	49.0	153	2	B27804	insulin-like growt
21	111	43.5	122	2	PN0622	insulin-like growt
22	96	37.6	193	2	A53697	insulin-like growt
23	90	35.3	181	2	A27804	insulin-like growt
24	88.5	34.7	195	1	IGHU1B	insulin-like growt
25	79.5	31.2	133	2	A40912	insulin-like growt
26	79.5	31.2	159	2	A26859	insulin-like growt
27	69.5	27.3	79	2	I51240	insulin-like growt
28	60.5	23.7	145	2	A87574	hypothetical prote
29	59	23.1	263	2	S64472	hypothetical prote
30	59	23.1	508	2	T22440	hypothetical prote
31	59	23.1	817	2	T22442	hypothetical prote
32	58	22.7	1106	2	JQ0405	hypothetical 119.5
33	58	22.7	1186	2	T19050	hypothetical prote
34	57.5	22.5	407	2	S53900	hypothetical prote
35	57.5	22.5	509	2	T31797	hypothetical prote
36	57	22.4	590	1	TVFFDS	protein-tyrosine k
37	57	22.4	751	1	TVVPTH	large T antigen -
38	56.5	22.2	1206	2	E86445	hypothetical prote
39	56	22.0	433	2	T46512	probable serine/th
40	56	22.0	816	2	T27189	hypothetical prote
41	55.5	21.8	321	2	S62015	SOL1 protein - yea
42	55.5	21.8	511	2	S58399	cellutagmin I sytV
43	55.5	21.8	564	2	A38271	serotonin receptor
44	55	21.6	55	1	VHNVAC	nucleocapsid prote
45	55	21.6	151	2	T43960	hypothetical prote

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-2.rup.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:14:17 ; Search time 113.421 Seconds
(without alignments)
292.359 Million cell updates/sec

Title: US-10-647-732A-2
Perfect score: 255
Sequence: 1 RSVRAQRHTDMPRTPKKPLS.....KEVHQKNSSRGNTGGRNYRM 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	255	100.0	161	2	Q91230_ONCTS	Q91230 oncorhynchu
2	237	92.9	161	2	Q90VV9_BRARE	Q90vv9 brachydanio
3	235	92.2	161	1	IGF1A_CYPKA	Q90325 cyprinus ca
4	234	91.8	159	2	Q6V293 ICTPU	Q6v293 ictalurus p
5	231.5	90.8	188	1	IGF1_ONCKI	P17085 oncorhynchu
6	231.5	90.8	188	2	Q91965_ONCTS	Q91965 oncorhynchu
7	225	88.2	161	2	Q506L8_9TELE	Q506l8 cirrhinus m
8	217	85.1	117	2	Q9I9I4_CTEID	Q9i9i4 ctenopharyn
9	217	85.1	161	2	Q800D5_9TELE	Q800d5 megalobrama
10	217	85.1	161	2	Q98SR6_MEGAM	Q98sr6 megalobrama
11	216	84.7	159	2	O93607_PAROL	O93607 paralichthy
12	216	84.7	178	2	Q5BQH3_9TELE	Q5bqh3 gymnocypris
13	214.5	84.1	160	2	Q70BT5_PERFL	Q70bt5 perca fluvi
14	212	83.1	161	2	Q9PWK2_CARAU	Q9pwk2 carassius a

15	212	83.1	161	2	Q9YI82_CARAU	Q9yi82 carassius a
16	211	82.7	161	1	IGF1B_CYPCA	Q90326 cyprinus ca
17	211	82.7	178	2	Q9IBI0_CYPCA	Q9ibi0 cyprinus ca
18	208.5	81.8	186	2	Q800Y5_SIGGU	Q800y5 siganus gut
19	198.5	77.8	186	2	Q5Q0U4_DICLA	Q5q0u4 dicentrarch
20	198.5	77.8	186	2	Q5U8T6_EPICO	Q5u8t6 epinephelus
21	198.5	77.8	186	2	Q6R527_EPICO	Q6r527 epinephelus
22	198.5	77.8	186	2	Q6T8S2_MUGCE	Q6t8s2 mugil cepha
23	198.5	77.8	186	2	Q70BT6_PERFL	Q70bt6 perca fluvi
24	198.5	77.8	186	2	Q7T1A7_PERFV	Q7t1a7 perca flave
25	198.5	77.8	186	2	Q9PSX5_PAROL	Q9psx5 paralichthy
26	194.5	76.3	186	2	O93527_PAROL	O93527 paralichthy
27	187.5	73.5	185	2	Q9YI57_ACASC	Q9yi57 acanthopagr
28	187.5	73.5	185	2	Q4G1F3_SPAAU	Q4g1f3 sparus aura
29	172	67.5	149	2	Q91231_ONCTS	Q91231 oncorhynchu
30	168.5	66.1	176	1	IGF1_ONCMY	Q02815 oncorhynchu
31	163.5	64.1	182	2	O42289_OREMO	O42289 oreochromis
32	163.5	64.1	182	2	O73720_OREMO	O73720 oreochromis
33	163.5	64.1	182	2	P79824_OREMO	P79824 oreochromis
34	160.5	62.9	184	2	O42336_MYOSC	O42336 myoxocephal
35	140	54.9	124	1	IGF1_COTJA	P51462 coturnix co
36	140	54.9	153	1	IGF1_CHICK	P18254 gallus gall
37	137	53.7	153	2	O93380_MELGA	O93380 meleagris g
38	132	51.8	130	1	IGF1_CAVPO	P17647 cavia porce
39	132	51.8	130	2	Q9NP10_HUMAN	Q9np10 homo sapien
40	132	51.8	137	2	Q14620_HUMAN	Q14620 homo sapien
41	132	51.8	153	1	IGF1A_HUMAN	P01343 homo sapien
42	132	51.8	153	2	Q5U743_HUMAN	Q5u743 homo sapien
43	132	51.8	184	2	Q59GC5_HUMAN	Q59gc5 homo sapien
44	131	51.4	153	1	IGF1_XENLA	P16501 xenopus lae
45	128	50.2	153	1	IGF1_PIG	P16545 sus scrofa

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:13:52 ; Search time 165.736 Seconds
 (without alignments)
 196.180 Million cell updates/sec

Title: US-10-647-732A-4
 Perfect score: 393
 Sequence: 1 RSVRAQRHTDMPRTPKVSTA.....KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	393	100.0	74	3	AAy77407	Aay77407 Rainbow t	
2	393	100.0	74	7	ADf56465	Adf56465 Rainbow t	
3	382	97.2	74	7	ADD67518	Add67518 Rainbow t	
4	382	97.2	74	8	ADp82540	Adp82540 Rainbow t	
5	326	83.0	186	2	AAR72472	Aar72472 Flatfish	
6	326	83.0	186	8	ADV95289	Adv95289 Rockfish	
7	299	76.1	62	3	AAy77406	Aay77406 Rainbow t	

8	299	76.1	62	7	ADD67519	Add67519	Rainbow t
9	299	76.1	62	7	ADF56464	Adf56464	Rainbow t
10	299	76.1	62	8	ADP82541	Adp82541	Rainbow t
11	299	76.1	176	2	AAR88089	Aar88089	Rainbow t
12	231.5	58.9	47	3	AA77405	Aay77405	Rainbow t
13	231.5	58.9	47	7	ADF56463	Adf56463	Rainbow t
14	220.5	56.1	47	7	ADD67520	Add67520	Rainbow t
15	220.5	56.1	47	8	ADP82542	Adp82542	Rainbow t
16	220	56.0	185	3	ABB06295	Abb06295	Paralicht
17	160	40.7	178	9	AEB07519	Aeb07519	Korean ro
18	158.5	40.3	35	3	AA77404	Aay77404	Rainbow t
19	158.5	40.3	35	7	ADD67521	Add67521	Rainbow t
20	158.5	40.3	35	7	ADF56462	Adf56462	Rainbow t
21	158.5	40.3	35	8	ADP82543	Adp82543	Rainbow t
22	118.5	30.2	105	4	AAE02452	Aae02452	Rabbit li
23	118.5	30.2	105	4	AAE02450	Aae02450	Human liv
24	118.5	30.2	105	4	AAE02456	Aae02456	Rabbit li
25	118.5	30.2	105	5	AAU10562	Aau10562	Human ins
26	118.5	30.2	105	5	AAU10564	Aau10564	Rabbit in
27	118.5	30.2	105	7	ABR63172	Abr63172	Rabbit li
28	118.5	30.2	105	7	ABR63170	Abr63170	Human liv
29	118.5	30.2	105	9	ADZ58808	Adz58808	Human mat
30	118.5	30.2	119	1	AAP60578	Aap60578	Human pre
31	118.5	30.2	130	9	AEB70451	Aeb70451	Insulin-l
32	118.5	30.2	137	4	AAU09067	Aau09067	Human ins
33	118.5	30.2	137	8	ADU46866	Adu46866	Insulin-l
34	118.5	30.2	137	9	AEB70455	Aeb70455	Insulin-l
35	118.5	30.2	137	9	AEB70450	Aeb70450	Insulin-l
36	118.5	30.2	153	2	AAR83803	Aar83803	Insulin-l
37	118.5	30.2	153	2	AAW69733	Aaw69733	Human IGF
38	118.5	30.2	153	2	AAW57882	Aaw57882	Human IGF
39	118.5	30.2	153	5	AAU84284	Aau84284	Human end
40	118.5	30.2	153	5	AAU84341	Aau84341	Protein I
41	118.5	30.2	153	6	ADA26451	Ada26451	Human ins
42	118.5	30.2	153	7	ADC59343	Adc59343	Human ins
43	118.5	30.2	153	7	ADD25494	Add25494	Binding d
44	118.5	30.2	153	7	ADP65213	Adp65213	Human ins
45	118.5	30.2	153	8	ADH10374	Adh10374	Human ins

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:23:52 ; Search time 40.9752 Seconds
 (without alignments)
 149.310 Million cell updates/sec

Title: US-10-647-732A-4
 Perfect score: 393
 Sequence: 1 RSVRAQRHTDMPRTPKVSTA.....KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result	% Query					
No.	Score	Match	Length	DB	ID	Description
1	393	100.0	74	2	US-09-120-818-4	Sequence 4, Appli
2	393	100.0	74	2	US-09-609-642-4	Sequence 4, Appli
3	393	100.0	74	2	US-09-669-642-4	Sequence 4, Appli
4	299	76.1	62	2	US-09-120-818-3	Sequence 3, Appli
5	299	76.1	62	2	US-09-609-642-3	Sequence 3, Appli
6	299	76.1	62	2	US-09-669-642-3	Sequence 3, Appli
7	299	76.1	176	1	US-07-953-230A-9	Sequence 9, Appli
8	231.5	58.9	47	2	US-09-120-818-2	Sequence 2, Appli
9	231.5	58.9	47	2	US-09-609-642-2	Sequence 2, Appli
10	231.5	58.9	47	2	US-09-669-642-2	Sequence 2, Appli

11	158.5	40.3	35	2	US-09-120-818-1	Sequence 1, Appli
12	158.5	40.3	35	2	US-09-609-642-1	Sequence 1, Appli
13	158.5	40.3	35	2	US-09-669-642-1	Sequence 1, Appli
14	118.5	30.2	105	2	US-09-852-261-10	Sequence 10, Appl
15	118.5	30.2	105	2	US-09-852-261-14	Sequence 14, Appl
16	118.5	30.2	119	6	5405942-1	Patent No. 5405942
17	118.5	30.2	127	2	US-09-617-389B-18	Sequence 18, Appl
18	118.5	30.2	137	1	US-07-953-230A-10	Sequence 10, Appl
19	118.5	30.2	152	2	US-08-950-720A-9	Sequence 9, Appli
20	118.5	30.2	153	1	US-08-219-878A-1	Sequence 1, Appli
21	118.5	30.2	153	2	US-09-917-254-82	Sequence 82, Appl
22	118.5	30.2	153	2	US-09-919-497-74	Sequence 74, Appl
23	118.5	30.2	153	4	PCT-US93-04329-1	Sequence 1, Appli
24	118.5	30.2	156	2	US-09-142-583A-11	Sequence 11, Appl
25	118.5	30.2	184	2	US-09-949-016-7523	Sequence 7523, Ap
26	118.5	30.2	191	2	US-08-989-251-41	Sequence 41, Appl
27	118.5	30.2	191	2	US-09-340-250-41	Sequence 41, Appl
28	118.5	30.2	191	2	US-09-528-108-41	Sequence 41, Appl
29	118.5	30.2	191	2	US-09-921-398-41	Sequence 41, Appl
30	118.5	30.2	191	2	US-10-280-826-41	Sequence 41, Appl
31	111.5	28.4	105	2	US-09-852-261-12	Sequence 12, Appl
32	83	21.1	110	2	US-09-852-261-2	Sequence 2, Appli
33	81	20.6	111	2	US-09-852-261-6	Sequence 6, Appli
34	81	20.6	121	2	US-09-142-583A-4	Sequence 4, Appli
35	79.5	20.2	454	2	US-09-080-044-4	Sequence 4, Appli
36	79.5	20.2	454	2	US-09-531-857A-4	Sequence 4, Appli
37	78	19.8	111	2	US-09-852-261-4	Sequence 4, Appli
38	74	18.8	19	2	US-09-142-583A-6	Sequence 6, Appli
39	68.5	17.4	312	2	US-09-252-991A-17496	Sequence 17496, A
40	65	16.5	212	2	US-09-252-991A-19925	Sequence 19925, A
41	64.5	16.4	186	2	US-09-252-991A-27476	Sequence 27476, A
42	64.5	16.4	216	2	US-09-252-991A-32065	Sequence 32065, A
43	64.5	16.4	389	2	US-09-949-016-6442	Sequence 6442, Ap
44	64.5	16.4	417	2	US-09-949-016-10594	Sequence 10594, A
45	63.5	16.2	429	2	US-09-252-991A-29079	Sequence 29079, A

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rapbm.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:24:43 ; Search time 145.554 Seconds
(without alignments)
212.426 Million cell updates/sec

Title: US-10-647-732A-4
Perfect score: 393
Sequence: 1 RSVRAQRHTDMPRTPKVSTA.....KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	382	97.2	74	4	US-10-100-492-2	Sequence 2, Appli
2	326	83.0	186	6	US-11-049-518-27	Sequence 27, Appl
3	299	76.1	62	4	US-10-100-492-3	Sequence 3, Appli
4	220.5	56.1	47	4	US-10-100-492-4	Sequence 4, Appli
5	158.5	40.3	35	4	US-10-100-492-5	Sequence 5, Appli
6	118.5	30.2	105	3	US-09-852-261-10	Sequence 10, Appl
7	118.5	30.2	105	3	US-09-852-261-14	Sequence 14, Appl
8	118.5	30.2	105	5	US-10-504-078-10	Sequence 10, Appl
9	118.5	30.2	105	5	US-10-504-078-14	Sequence 14, Appl
10	118.5	30.2	105	5	US-10-688-821-53	Sequence 53, Appl

11	118.5	30.2	127	4	US-10-700-725-18	Sequence 18, Appl
12	118.5	30.2	130	6	US-11-049-518-25	Sequence 25, Appl
13	118.5	30.2	137	4	US-10-251-661-8	Sequence 8, Appli
14	118.5	30.2	153	3	US-09-919-497-74	Sequence 74, Appl
15	118.5	30.2	153	3	US-09-861-101-5	Sequence 5, Appli
16	118.5	30.2	153	4	US-10-136-639-3	Sequence 3, Appli
17	118.5	30.2	153	4	US-10-207-655-55	Sequence 55, Appl
18	118.5	30.2	153	4	US-10-460-550-5	Sequence 5, Appli
19	118.5	30.2	153	4	US-10-706-791-2	Sequence 2, Appli
20	118.5	30.2	153	5	US-10-851-921-2	Sequence 2, Appli
21	118.5	30.2	153	5	US-10-461-862-68	Sequence 68, Appl
22	118.5	30.2	153	5	US-10-460-550-5	Sequence 5, Appli
23	118.5	30.2	153	5	US-10-287-436A-455	Sequence 455, App
24	118.5	30.2	153	5	US-10-287-436A-1154	Sequence 1154, Ap
25	118.5	30.2	153	5	US-10-798-896-4	Sequence 4, Appli
26	118.5	30.2	191	3	US-09-921-398-41	Sequence 41, Appl
27	118.5	30.2	191	3	US-09-967-768-41	Sequence 41, Appl
28	118.5	30.2	191	4	US-10-280-826-41	Sequence 41, Appl
29	118.5	30.2	191	6	US-11-046-099-41	Sequence 41, Appl
30	113.5	28.9	105	4	US-10-238-114-3	Sequence 3, Appli
31	113.5	28.9	153	4	US-10-238-114-2	Sequence 2, Appli
32	111.5	28.4	105	3	US-09-852-261-12	Sequence 12, Appl
33	111.5	28.4	105	5	US-10-504-078-12	Sequence 12, Appl
34	93	23.7	77	4	US-10-100-492-1	Sequence 1, Appli
35	93	23.7	195	4	US-10-443-466A-20	Sequence 20, Appl
36	93	23.7	195	4	US-10-706-791-3	Sequence 3, Appli
37	93	23.7	195	5	US-10-461-862-66	Sequence 66, Appl
38	83	21.1	110	3	US-09-852-261-2	Sequence 2, Appli
39	83	21.1	110	5	US-10-504-078-2	Sequence 2, Appli
40	81	20.6	111	3	US-09-852-261-6	Sequence 6, Appli
41	81	20.6	111	5	US-10-504-078-6	Sequence 6, Appli
42	80	20.4	104	6	US-11-049-518-17	Sequence 17, Appl
43	78	19.8	111	3	US-09-852-261-4	Sequence 4, Appli
44	78	19.8	111	5	US-10-504-078-4	Sequence 4, Appli
45	78	19.8	133	4	US-10-161-088-2	Sequence 2, Appli

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rapbn.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:25:58 ; Search time 20.7934 Seconds
(without alignments)
156.599 Million cell updates/sec

Title: US-10-647-732A-4
Perfect score: 393
Sequence: 1 RSVRAQRHTDMPRTPKVSTA.....KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	393	100.0	74	6	US-10-647-732A-4	Sequence 4, Appli
2	299	76.1	62	6	US-10-647-732A-3	Sequence 3, Appli
3	231.5	58.9	47	6	US-10-647-732A-2	Sequence 2, Appli
4	158.5	40.3	35	6	US-10-647-732A-1	Sequence 1, Appli
5	118.5	30.2	105	7	US-11-228-458-10	Sequence 10, Appl
6	118.5	30.2	105	7	US-11-228-458-14	Sequence 14, Appl
7	118.5	30.2	130	7	US-11-043-788-222	Sequence 222, App
8	118.5	30.2	137	7	US-11-043-788-221	Sequence 221, App

9	118.5	30.2	137	7	US-11-043-788-226	Sequence 226, App
10	118.5	30.2	153	7	US-11-043-788-223	Sequence 223, App
11	118.5	30.2	153	7	US-11-043-788-228	Sequence 228, App
12	118.5	30.2	153	7	US-11-244-925-4	Sequence 4, Appli
13	118.5	30.2	567	6	US-10-954-468-8	Sequence 8, Appli
14	118.5	30.2	574	6	US-10-954-468-4	Sequence 4, Appli
15	118.5	30.2	580	6	US-10-954-468-6	Sequence 6, Appli
16	118.5	30.2	587	6	US-10-954-468-2	Sequence 2, Appli
17	118.5	30.2	615	6	US-10-954-468-7	Sequence 7, Appli
18	118.5	30.2	622	6	US-10-954-468-3	Sequence 3, Appli
19	118.5	30.2	628	6	US-10-954-468-5	Sequence 5, Appli
20	118.5	30.2	633	6	US-10-954-468-1	Sequence 1, Appli
21	111.5	28.4	105	7	US-11-228-458-12	Sequence 12, Appl
22	93	23.7	195	7	US-11-043-788-220	Sequence 220, App
23	93	23.7	195	7	US-11-043-788-227	Sequence 227, App
24	83	21.1	110	7	US-11-228-458-2	Sequence 2, Appli
25	83	21.1	139	7	US-11-043-788-224	Sequence 224, App
26	83	21.1	142	7	US-11-043-788-225	Sequence 225, App
27	81	20.6	111	7	US-11-228-458-6	Sequence 6, Appli
28	78	19.8	111	7	US-11-228-458-4	Sequence 4, Appli
29	74	18.8	19	7	US-11-043-788-487	Sequence 487, App
30	66	16.8	430	7	US-11-096-568A-25863	Sequence 25863, A
31	62.5	15.9	144	7	US-11-096-568A-19656	Sequence 19656, A
32	62.5	15.9	155	7	US-11-096-568A-19655	Sequence 19655, A
33	62.5	15.9	218	7	US-11-096-568A-19654	Sequence 19654, A
34	62.5	15.9	330	7	US-11-188-298-2721	Sequence 2721, Ap
35	62.5	15.9	1158	6	US-10-501-035-366	Sequence 366, App
36	62.5	15.9	1158	7	US-11-075-646-6	Sequence 6, Appli
37	62	15.8	346	6	US-10-467-657-2676	Sequence 2676, Ap
38	62	15.8	800	7	US-11-087-099-11477	Sequence 11477, A
39	62	15.8	948	6	US-10-523-477-14	Sequence 14, Appl
40	61.5	15.6	260	7	US-11-096-568A-19639	Sequence 19639, A
41	61.5	15.6	370	7	US-11-096-568A-28786	Sequence 28786, A
42	61.5	15.6	494	7	US-11-096-568A-28785	Sequence 28785, A
43	61.5	15.6	506	7	US-11-096-568A-28784	Sequence 28784, A
44	61.5	15.6	1009	6	US-10-514-531-11	Sequence 11, Appl
45	61	15.5	643	7	US-11-137-465-54	Sequence 54, Appl

SCORE Search Results Details for Application
10647732 and Search Result us-10-647-732a-
4.rpr.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:19:02 ; Search time 29.9669 Seconds
(without alignments)
237.596 Million cell updates/sec

Title: US-10-647-732A-4
Perfect score: 393
Sequence: 1 RSVRAQRHTDMPRTPKVSTA.....KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	393	100.0	188	2	A54270	insulin-like growt
2	393	100.0	188	2	B54270	insulin-like growt

3	347	88.3	155	2	C44012	insulin-like growt
4	304	77.4	176	2	A41396	insulin-like growt
5	299	76.1	176	2	A46244	insulin-like growt
6	231.5	58.9	161	2	C54270	insulin-like growt
7	207.5	52.8	79	2	I51240	insulin-like growt
8	174.5	44.4	193	2	A53697	insulin-like growt
9	158.5	40.3	149	2	D54270	insulin-like growt
10	126.5	32.2	153	2	A41399	insulin-like growt
11	118.5	30.2	137	1	IGGP1	insulin-like growt
12	118.5	30.2	137	2	A36552	insulin-like growt
13	118.5	30.2	153	1	IGHU1	insulin-like growt
14	117.5	29.9	153	2	A36079	insulin-like growt
15	114.5	29.1	153	2	S12825	insulin-like growt
16	113.5	28.9	138	2	S22878	insulin-like growt
17	113.5	28.9	153	1	IGBO1	insulin-like growt
18	113.5	28.9	154	2	JC2483	insulin-like growt
19	113.5	28.9	154	2	A33390	insulin-like growt
20	111.5	28.4	127	2	B40912	insulin-like growt
21	111.5	28.4	127	2	A25540	insulin-like growt
22	111.5	28.4	153	2	B27804	insulin-like growt
23	97.5	24.8	122	2	PN0622	insulin-like growt
24	93	23.7	195	1	IGHU1B	insulin-like growt
25	82.5	21.0	181	2	A27804	insulin-like growt
26	78	19.8	133	2	A40912	insulin-like growt
27	78	19.8	159	2	A26859	insulin-like growt
28	75.5	19.2	129	2	G36790	hypothetical prote
29	70.5	17.9	190	2	JC6062	ribosomal protein
30	69	17.6	1937	2	T03224	probable polyketid
31	68.5	17.4	212	2	C70898	hypothetical prote
32	67.5	17.2	1791	2	T02345	hypothetical prote
33	66.5	16.9	291	2	T27534	hypothetical prote
34	66	16.8	551	2	C84549	probable ubiquitin
35	66	16.8	1500	2	T03824	probable immediate
36	65.5	16.7	1148	2	T09073	splicing factor Si
37	64	16.3	234	2	T45709	hypothetical prote
38	64	16.3	263	2	S64857	hypothetical prote
39	64	16.3	535	2	C36811	hypothetical prote
40	64	16.3	535	2	A37994	RF1 protein - saim
41	63.5	16.2	310	2	S36581	E2 protein - human
42	63.5	16.2	483	2	F71619	hypothetical prote
43	63.5	16.2	2441	2	D71623	erythrocyte membra
44	63	16.0	489	2	T26069	hypothetical prote
45	63	16.0	1762	2	T03222	probable polyketid

This page gives you Search Results detail for the Application 10647732 and Search Result us-10-647-732a-4.rup.

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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:14:17 ; Search time 178.579 Seconds
(without alignments)
292.359 Million cell updates/sec

Title: US-10-647-732A-4
Perfect score: 393
Sequence: 1 RSVRAQRHTDMPRTPKVSTA.....KEVHQKNSSRGNTGGRNYRM 74

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	393	100.0	188	2	Q91965_ONCTS	Q91965 oncorhynchu
2	387	98.5	188	1	IGF1_ONCKI	P17085 oncorhynchu
3	337	85.8	186	2	Q800Y5_SIGGU	Q800y5 siganus gut
4	329	83.7	186	2	O93527_PAROL	O93527 paralichthy
5	326	83.0	186	2	Q5Q0U4_DICLA	Q5q0u4 dicentrarch
6	326	83.0	186	2	Q5U8T6_EPICO	Q5u8t6 epinephelus
7	326	83.0	186	2	Q6R527_EPICO	Q6r527 epinephelus
8	326	83.0	186	2	Q70BT6_PERFL	Q70bt6 perca fluvi
9	326	83.0	186	2	Q7T1A7_PERFV	Q7t1a7 perca flave
10	326	83.0	186	2	Q9PSX5_PAROL	Q9psx5 paralichthy
11	321	81.7	186	2	Q6T8S2_MUGCE	Q6t8s2 mugil cepha
12	315	80.2	185	2	Q9YI57_ACASC	Q9yi57 acanthopagr
13	315	80.2	185	2	Q4G1F3_SPAAU	Q4g1f3 sparus aura
14	299	76.1	176	1	IGF1_ONCMY	Q02815 oncorhynchu

15	270	68.7	184	2	O42336_MYOSC	O42336 myoxocephal
16	258	65.6	182	2	O73720_OREMO	O73720 oreochromis
17	258	65.6	182	2	P79824_OREMO	P79824 oreochromis
18	251	63.9	182	2	O42289_OREMO	O42289 oreochromis
19	231.5	58.9	161	2	Q91230_ONCTS	Q91230 oncorhynchu
20	220	56.0	185	2	O57436_PAROL	O57436 paralichthy
21	213.5	54.3	161	2	Q90VV9_BRARE	Q90vv9 brachydanio
22	211.5	53.8	161	1	IGF1A_CYPKA	Q90325 cyprinus ca
23	210.5	53.6	159	2	Q6V293 ICTPU	Q6v293 ictalurus p
24	207.5	52.8	79	2	P81416_ONCKE	P81416 oncorhynchu
25	204.5	52.0	161	2	Q506L8_9TELE	Q506l8 cirrhinus m
26	204	51.9	160	2	Q70BT5_PERFL	Q70bt5 perca fluvi
27	196.5	50.0	117	2	Q9I9I4_CTEID	Q9i9i4 ctenopharyn
28	196.5	50.0	161	2	Q800D5_9TELE	Q800d5 megalobrama
29	196.5	50.0	161	2	Q98SR6_MEGAM	Q98sr6 megalobrama
30	192.5	49.0	159	2	O93607_PAROL	O93607 paralichthy
31	192.5	49.0	161	2	Q9PWK2_CARAU	Q9pwk2 carassius a
32	192.5	49.0	161	2	Q9YI82_CARAU	Q9yi82 carassius a
33	192.5	49.0	178	2	Q5BQH3_9TELE	Q5bqh3 gymnocypris
34	187.5	47.7	161	1	IGF1B_CYPKA	Q90326 cyprinus ca
35	187.5	47.7	178	2	Q9IBI0_CYPKA	Q9ibi0 cyprinus ca
36	174.5	44.4	193	2	Q7LZC6_CLAMA	Q7lzc6 clarias mac
37	158.5	40.3	149	2	Q91231_ONCTS	Q91231 oncorhynchu
38	126.5	32.2	124	1	IGF1_COTJA	P51462 coturnix co
39	126.5	32.2	153	1	IGF1_CHICK	P18254 gallus gall
40	123.5	31.4	153	2	O93380_MELGA	O93380 meleagris g
41	118.5	30.2	130	1	IGF1_CAVPO	P17647 cavia porce
42	118.5	30.2	130	2	Q9NP10_HUMAN	Q9np10 homo sapien
43	118.5	30.2	137	2	Q14620_HUMAN	Q14620 homo sapien
44	118.5	30.2	153	1	IGF1A_HUMAN	P01343 homo sapien
45	118.5	30.2	153	2	Q5U743_HUMAN	Q5u743 homo sapien